

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/497,957

DATE: 10/14/2000
 TIME: 01:10:52

INPUT SET: S36007.raw

**This Raw Listing contains the General
 Information Section and up to the first 5 pages.**

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SEQUENCE LISTING

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(1) General Information:

- (i) APPLICANT: Thomas, Winston J.
 Drayna, Dennis T.
 Feder, John N.
 Gnirke, Andreas
 Ruddy, David
 Tsuchihashi, Zenta
 Wolff, Roger K.

(ii) TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS

(iii) NUMBER OF SEQUENCES: 76

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Pennie & Edmonds LLP
- (B) STREET: 1155 Avenue of the Americas
- (C) CITY: New York
- (D) STATE: New York
- (E) COUNTRY: USA
- (F) ZIP: 10036-2811

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: Windows 95
- (D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/497,957
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US/08/834,497
- (B) FILING DATE: 04-APR-1997

- (A) APPLICATION NUMBER: US 08/652,265
- (B) FILING DATE: 23-MAY-1996

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/632,673
- (B) FILING DATE: 16-APR-1996

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(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/630,912
- (B) FILING DATE: 04-APR-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Poissant, Brian M.
- (B) REGISTRATION NUMBER: 28,462
- (C) REFERENCE/DOCKET NUMBER: 8907-0056-999

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(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650-493-4935
- (B) TELEFAX: 650-493-5556
- (C) TELEX: 66141 PENNIE

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881, 6040..6153, 7107..7147)
- (D) OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein"
/note= "Normal or wild-type (unaffected) Hereditary Hemochromatosis (HH) gene allele"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 140..7319
- (D) OTHER INFORMATION: /note= "start and stop positions for normal or wild-type (unaffected) allele cDNA (SEQ ID NO:9)"

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 3852..3891
- (D) OTHER INFORMATION: /note= "start and stop positions for normal or wild-type (unaffected) genomic sequence surrounding variant for 24d2(C) allele (SEQ ID NO:41)"

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100 (ix) FEATURE:
101 (A) NAME/KEY: -
102 (B) LOCATION: 5507..6023
103 (D) OTHER INFORMATION: /note= "start and stop positions for
104 normal or wild-type (unaffected) genomic
105 sequence surrounding variant for 24d1(G)
106 allele (SEQ ID NO:20)"
107

108 (ix) FEATURE:
109 (A) NAME/KEY: allele
110 (B) LOCATION: replace(3872, "c")
111 (D) OTHER INFORMATION: /phenotype= "normal or wild-type
112 (unaffected)"
113 /label= 24d2
114

115 (ix) FEATURE:
116 (A) NAME/KEY: allele
117 (B) LOCATION: replace(3878, "a")
118 (D) OTHER INFORMATION: /phenotype= "normal or wild-type
119 (unaffected)"
120 /label= 24d7
121

122 (ix) FEATURE:
123 (A) NAME/KEY: allele
124 (B) LOCATION: replace(5834, "g")
125 (D) OTHER INFORMATION: /phenotype= "normal or wild-type
126 (unaffected)"
127 /label= 24d1
128
129

130 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

131
132 TCTAAGGTTG AGATAAAATT TTAAATGTA TGATTGAATT TTGAAAATCA TAAATATTTA 60
133
134 AATATCTAAA GTTCAGATCA GAACATTGCG AAGCTACTTT CCCCAATCAA CAACACCCCT 120
135
136 TCAGGATTTA AAAACCAAGG GGGACACTGG ATCACCTAGT GTTTCACAAG CAGGTACCTT 180
137
138 CTGCTGTAGG AGAGAGAGAA CTAAAGTTCT GAAAGACCTG TTGCTTTTCA CCAGGAAGTT 240
139
140 TTAAGTGGCA TCTCCTGAGC CTAGGCAATA GCTGTAGGGT GACTTCTGGA GCCATCCCCG 300
141
142 TTTCCCCGCC CCCCAAAGA AGCGGAGATT TAACGGGGAC GTGCGGCCAG AGCTGGGGAA 360
143
144 ATG GGC CCG CGA GCC AGG CCG GCG CTT CTC CTC CTG ATG CTT TTG CAG 408
145 Met Gly Pro Arg Ala Arg Pro Ala Leu Leu Leu Leu Met Leu Leu Gln
146 1 5 10 15
147
148 ACC GCG GTC CTG CAG GGG CGC TTG CTG C GTGAGTCCGA GGGCTGCGGG 456
149 Thr Ala Val Leu Gln Gly Arg Leu Leu
150 20 25
151
152 CGAACTAGGG GCGCGGCGGG GGTGGAAAAA TCGAACTAG CTTTTTCTTT GCGCTTGGGA 516

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153							
154	GTTTGCTAAC	TTTGGAGGAC	CTGCTCAACC	CTATCCGCAA	GCCCCCTCTCC	CTACTTTCTG	576
155							
156	CGTCCAGACC	CCGTGAGGGA	GTGCCTACCA	CTGAACTGCA	GATAGGGGTC	CCTCGCCCCA	636
157							
158	GGACCTGCCC	CCTCCCCCGG	CTGTCCC GGC	TCTGCGGAGT	GACTTTTGGGA	ACCGCCCCACT	696
159							
160	CCCTTCCCCC	AACTAGAATG	CTTTTAAATA	AATCTCGTAG	TTCCTCACTT	GAGCTGAGCT	756
161							
162	AAGCCTGGGG	CTCCTTGAAC	CTGGAAC TCG	GGTTTATTTT	CAATGTCAGC	TGTGCAGTTT	816
163							
164	TTTCCCCAGT	CATCTCCAAA	CAGGAAGTTC	TTCCCTGAGT	GCTTGCCGAG	AAGGCTGAGC	876
165							
166	AAACCCACAG	CAGGATCCGC	ACGGGGTTTC	CACCTCAGAA	CGAATGCGTT	GGGCGGTGGG	936
167							
168	GGCGCGAAAG	AGTGGCGTTG	GGGATCTGAA	TTCTTCACCA	TTCCACCCAC	TTTTGGTGAG	996
169							
170	ACCTGGGGTG	GAGGTCTCTA	GGGTGGGAGG	CTCCTGAGAG	AGGCCTACCT	CGGGCCTTTC	1056
171							
172	CCCAC TCTG	GCAATTGTTT	TTTTGCCTGG	AAAATTAAGT	ATATGTTAGT	TTTGAACGTT	1116
173							
174	TGAACTGAAC	AATTCTCTTT	TCGGCTAGGC	TTTATTGATT	TGCAATGTGC	TGTGTAATTA	1176
175							
176	AGAGGCCCTCT	CTACAAAGTA	CTGATAATGA	ACATGTAAGC	AATGCACTCA	CTTCTAAGTT	1236
177							
178	ACATTCATAT	CTGATCTTAT	TTGATTTTCA	CTAGGCATAG	GGAGGTAGGA	GCTAATAATA	1296
179							
180	CGTTTATTTT	ACTAGAAGTT	AACTGGAATT	CAGATTATAT	AACTCTTTTC	AGGTTACAAA	1356
181							
182	GAACATAAAT	AATCTGGTTT	TCTGATGTTA	TTTCAAGTAC	TACAGCTGCT	TCTAATCTTA	1416
183							
184	GTTGACAGTG	ATTTTGGCCT	GTAGTGTAGC	ACAGTGTTCT	GTGGGTCACA	CGCCGGCCTC	1476
185							
186	AGCACAGCAC	TTTGAGTTTT	GGTACTACGT	GTATCCACAT	TTTACACATG	ACAAGAATGA	1536
187							
188	GGCATGGCAC	GGCCTGCTTC	CTGGCAAATT	TATTCAATGG	TACACTGGGC	TTTGGTGGCA	1596
189							
190	GAGCTCATGT	CTCCACTTCA	TAGCTATGAT	TCTTAAACAT	CACACTGCAT	TAGAGGTTGA	1656
191							
192	ATAATAAAAT	TTCATGTTGA	GCAGAAATAT	TCATTGTTTA	CAAGTGTAAG	TGAGTCCCAG	1716
193							
194	CCATGTGTTG	CACTGTTCAA	GCCCCAAGGG	AGAGAGCAGG	GAAACAAGTC	TTTACCCTTT	1776
195							
196	GATATTTTGC	ATTCTAGTGG	GAGAGATGAC	AATAAGCAAA	TGAGCAGAAA	GATATACAAC	1836
197							
198	ATCAGGAAAT	CATGGGTGTT	GTGAGAAGCA	GAGAAGTCAG	GGCAAGTCAC	TCTGGGGCTG	1896
199							
200	AACTTGAGC	AGAGACATGA	AGGAAATAAG	AATGATATTG	ACTGGGAGCA	GTATTTCCCA	1956
201							
202	GGCAAAC TGA	GTGGGCCTGG	CAAGTTGGAT	TAAAAAGCGG	GTTTTCTCAG	CACTACTCAT	2016
203							
204	GTGTGTGTGT	GTGGGGGGGG	GGGGCGGCGT	GGGGGTGGGA	AGGGGGACTA	CCATCTGCAT	2076
205							

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206	GTAGGATGTC	TAGCAGTATC	CTGTCCTCCC	TACTCACTAG	GTGCTAGGAG	CACTCCCCCA	2136
207							
208	GTCTTGACAA	CCAAAAATGT	CTCTAAACTT	TGCCACATGT	CACCTAGTAG	ACAAACTCCT	2196
209							
210	GGTTAAGAAG	CTCGGGTTGA	AAAAAATAAA	CAAGTAGTGC	TGGGGAGTAG	AGGCCAAGAA	2256
211							
212	GTAGGTAATG	GGCTCAGAAG	AGGAGCCACA	AACAAGGTTG	TGCAGGCGCC	TGTAGGCTGT	2316
213							
214	GGTGTGAATT	CTAGCCAAGG	AGTAACAGTG	ATCTGTCACA	GGCTTTTAAA	AGATTGCTCT	2376
215							
216	GGCTGCTATG	TGAAAGCAG	AATGAAGGGA	GCAACAGTAA	AAGCAGGGAG	CCCAGCCAGG	2436
217							
218	AAGCTGTTAC	ACAGTCCAGG	CAAGAGGTAG	TGGAGTGGGC	TGGGTGGGAA	CAGAAAAGGG	2496
219							
220	AGTGACAAAC	CATTGTCTCC	TGAATATATT	CTGAAGGAAG	TTGCTGAAGG	ATTCTATGTT	2556
221							
222	GTGTGAGAGA	AAGAGAAGAA	TTGGCTGGGT	GTAGTAGCTC	ATGCCAAGGA	GGAGGCCAAG	2616
223							
224	GAGAGCAGAT	TCCTGAGCTC	AGGAGTTCAA	GACCAGCCTG	GGCAACACAG	CAAAACCCCT	2676
225							
226	TCTCTACAAA	AAATACAAAA	ATTAGCTGGG	TGTGGTGGCA	TGCACCTGTG	ATCCTAGCTA	2736
227							
228	CTCGGGAGGC	TGAGGTGGAG	GGTATTGCTT	GAGCCAGGA	AGTTGAGGCT	GCAGTGAGCC	2796
229							
230	ATGACTGTGC	CACTGTACTT	CAGCCTAGGT	GACAGAGCAA	GACCCGTGTCT	CCCCTGACCC	2856
231							
232	CCTGAAAAAG	AGAAGAGTTA	AAGTTGACTT	TGTTCTTTAT	TTTAATTTTA	TTGGCCTGAG	2916
233							
234	CAGTGGGGTA	ATTGGCAATG	CCATTTCTGA	GATGGTGAAG	GCAGAGGAAA	GAGCAGTTTG	2976
235							
236	GGGTAAATCA	AGGATCTGCA	TTTGGGACAT	GTTAAGTTTG	AGATTCCAGT	CAGGCTTCCA	3036
237							
238	AGTGGTGAGG	CCACATAGGC	AGTTCAGTGT	AAGAATTCAG	GACCAAGGCT	GGGCACGGTG	3096
239							
240	GCTCACTTCT	GTAATCCCAG	CACTTTGGTG	GCTGAGGCAG	GTAGATCATT	TGAGGTCAGG	3156
241							
242	AGTTTGAGAC	AAGCTTGGCC	AACATGGTGA	AACCCCATGT	CTACTAAAAA	TACAAAAAAT	3216
243							
244	AGCCTGGTGT	GGTGGCGCAC	GCCTATAGTC	CCAGGTTTTT	AGGAGGCTTA	GGTAGGAGAA	3276
245							
246	TCCCTTGAAC	CCAGGAGGTG	CAGGTTGCAG	TGAGCTGAGA	TTGTGCCACT	GCACTCCAGC	3336
247							
248	CTGGGTGATA	GAGTGAGACT	CTGTCTCAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAACTGA	3396
249							
250	AGGAATTATT	CCTCAGGATT	TGGGTCTAAT	TTGCCCTGAG	CACCAACTCC	TGAGTTCAAC	3456
251							
252	TACCATGGCT	AGACACACCT	TAACATTTTC	TAGAATCCAC	CAGCTTTAGT	GGAGTCTGTC	3516
253							
254	TAATCATGAG	TATTGGAATA	GGATCTGGGG	GCAGTGAGGG	GGTGGCAGCC	ACGTGTGGCA	3576
255							
256	GAGAAAAGCA	CACAAGGAAA	GAGCACCCAG	GACTGTCATA	TGGAAGAAAG	ACAGGACTGC	3636
257							
258	AACTCACCCCT	TCACAAAATG	AGGACCAGAC	ACAGCTGATG	GTATGAGTTG	ATGCAGGTGT	3696



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2	XT/	1

Total number of pages: 2

Remarks:

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